

SEQUENCE LISTING

<110> FOGHER, CORRADO

<120> A SYNTHETIC POLYNUCLEOTIDE CODING FOR HUMAN
LACTOFERRIN, VECTORS, CELLS AND TRANSGENIC PLANTS
CONTAINING IT

<130> 618484-4/JP/B-4075PCT

<140> 09/743,823

<141> 2001-01-16

<150> IT RM98A000478

<151> 1998-07-17

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 2079

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA
encoding human lactoferrin

<220>

<221> CDS

<222> (1)..(2076)

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gcc	aca	aaa	tgc	ttc	caa	tgg	caa	agg	aat	atg	aga	aaa	gtt	cg	gga	96
Ala	Thr	Lys	Cys	Phe	Gln	Trp	Gln	Arg	Asn	Met	Arg	Lys	Val	Arg	Gly	
			20					25					30			

cct	cct	gta	tct	tgc	ata	aag	aga	gat	tca	ccc	atc	cag	tgt	atc	cag	144
Pro	Pro	Val	Ser	Cys	Ile	Lys	Arg	Asp	Ser	Pro	Ile	Gln	Cys	Ile	Gln	
		35						40				45				

gca	att	gcg	gaa	aac	aga	gct	gat	gct	gtg	act	ctt	gat	ggt	ggt	ttc	192
Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly	Gly	Phe	
	50					55				60						

ata	tac	gag	gca	gga	ctt	gcc	cca	tac	aaa	ctg	cga	cct	gta	gcg	gcg	240
Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val	Ala	Ala	
65					70					75					80	

gaa	gtc	tac	ggg	acc	gaa	aga	caa	cca	cga	act	cac	tat	tat	gct	gtg	288
Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr	Ala	Val	
				85					90					95		

gct gtt gtg aag aag ggc gga tct ttt cag ctg aac gaa ctt caa ggt Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly 100 105 110	336
ctg aag tca tgc cac aca gga ctt cgc agg acc gct gga tgg aat gtc Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val 115 120 125	384
cct ata ggg aca ctt cgt cca ttc ttg aat tgg acg ggt cca cct gag Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu 130 135 140	432
ccc att gag gca gct gtg gca aga ttc ttc tca gcc tct tgt gtt cca Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro 145 150 155 160	480
ggg gca gat aaa gga caa ttc ccc aac ctt tgt cgc ctg tgt gcg ggg Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly 165 170 175	528
aca ggg gaa aac aaa tgt gca ttc tca tcc cag gaa ccg tac ttc agc Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser 180 185 190	576
tac tct ggt gcc ttt aag tgt ctt aga gac ggt gct gga gat gtt gct Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala 195 200 205	624
ttt att aga gag agc aca gtg ttt gag gat ctt tca gac gag gct gaa Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu 210 215 220	672
agg gac gag tat gag tta ctc tgc cca gac aac act cgt aag cca gtt Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val 225 230 235 240	720
gac aag ttc aaa gat tgc cat ctt gca cgg gtc cct tct cat gcc gtt Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val 245 250 255	768
gtg gca cga agt gtt aat gga aag gag gat gcc atc tgg aat ctt ctc Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu 260 265 270	816
cgc caa gca cag gaa aag ttt gga aag gac aag tca ccg aaa ttc cag Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln 275 280 285	864
ctc ttt ggt tcc cct agt ggg cag aaa gat ctt ctg ttc aag gac tct Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser 290 295 300	912
gcc att ggg ttt tcg aga gtg cca cct agg ata gat tct ggg ttg tac Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr 305 310 315 320	960

ctt ggc tcc gga tac ttt act gca att cag aac ttg agg aaa agt gag	1008
Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu	
325 330 335	
gag gaa gtt gct gcc cgg cgt gcg cgg gtc gtt tgg tgt gcg gtg gga	1056
Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly	
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Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly	
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Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu	
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Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val	
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tac act gca ggt aaa tgt ggt ttg gtg cct gtc ctt gca gag aac tac	1248
Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr	
405 410 415	
aaa tca caa caa agc agt gac cct gat cct aac tgt gtg gat aga cct	1296
Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro	
420 425 430	
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Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser	
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Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val	
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Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln	
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acg ggc tcc tgc aaa ttt gat gaa tat ttc agt caa agc tgt gcc cct	1488
Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro	
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ggt tct gac cca aga tct aat ctc tgt gct ttg tgt att gga gat gag	1536
Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu	
500 505 510	
caa ggt gag aat aag tgc gtt ccc aac agc aac gag aga tac tac ggt	1584
Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly	
515 520 525	
tac act ggg gct ttc cgt tgc ttg gct gag aat gct gga gac gtt gca	1632
Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala	
530 535 540	

ttt gtg aaa gat gtc act gtc ttg cag aac act gat gga aat aac aat	1680
Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn	
545 550 555 560	
gag gca tgg gct aag gat ttg aag ctt gca gac ttt gcg ttg ctg tgc	1728
Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys	
565 570 575	
ctc gat ggc aaa cgt aag cct gtg act gaa gct aga agc tgc cat ctt	1776
Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu	
580 585 590	
gcc atg gcc ccg aat cat gct gtg gtg tct cgt atg gat aag gtg gaa	1824
Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu	
595 600 605	
cgc ttg aaa cag gtg ttg ctc cac caa cag gct aaa ttt ggt aga aat	1872
Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn	
610 615 620	
gga tct gac tgc ccg gac aag ttt tgc tta ttc cag tct gaa acc aaa	1920
Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys	
625 630 635 640	
aac ctt ttg ttc aat gac aac act gag tgt ctt gcc aga ctc cat ggc	1968
Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly	
645 650 655	
aaa aca aca tat gaa aaa tat ttg gga cca cag tat gtc gca ggc att	2016
Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile	
660 665 670	
act aat ctg aaa aag tgc tca acc tcc cca ctc cta gaa gcc tgt gaa	2064
Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu	
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Phe Leu Arg Lys	
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

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<210> 3

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 3

gagctccttc ggttttactt cctgaggaat tc

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<210> 4

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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tctagataaa ataatctata cattaaaaaa tttgatttta aa

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<210> 5

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

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ggatccgact gagtcggata agaagaaaag aaaaga

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<210> 6

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 6

tctagagttt tcaaatttga attttaatgt gtgttg

36

<210> 7

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 7

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36

<210> 8

<211> 250

<212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic DNA

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 gattcaccca tccagtgtat ccaggcaatt gcggaaaaca gagctgatgc tgtgactctt 180
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 gaagtctacg 250

<210> 9
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

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 ctgcgaagtc ctgtgtggca tgacttcaga ccttgaagtt cgttcagctg aaaagatccg 180
 cccttcttca caacagccac agcataatag tgagttcgtg gttgtctttc ggtcccgtag 240
 acttcgcccg 250

<210> 10
 <211> 250
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

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 aagacactta aaggcaccag agtagctgaa gtacggttcc tgggatgaga atgcacattt 180
 gttttcccct gtccccgcac acaggcgaca aaggttgggg aattgtcctt tatctgcacc 240
 tggaacacaa 250

<210> 11
 <211> 255
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400> 11
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 tccaaacttt tctgtgtgctt ggcggagaag attccagatg gcatcctcct ttccattaac 180

acttcgtgcc acaacggcat gagaaggac ccgtgcaaga tggcaatctt tgaacttgtc 240
aactggccta cgagt 255

<210> 12
<211> 251
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 12
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cacttgcgca actcttgctc tcccaccgca caccaaacga cccgcgcacg ccgggcagca 180
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aaccagaat c 251

<210> 13
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 13
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ttatccgact cagtc 75

<210> 14
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 14
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gtctcatttg gcattgcgta ttgggaaaag cagaaccca gtcacaacaa gtgcctccga 120
agttgcaata gcgagaaaga ctctacagg aaccaagcat gccacgctcg ttgcaacctc 180
cttaagggtg 189

<210> 15
<211> 250
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 15
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aagatatcct tccacaggtc tatccacaca gttaggatca gggtcactgc tttgttgtga 180
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ccatccaaac 250

<210> 16
<211> 254
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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ttattctcac cttgtctatc tccaatacac aaagcacaga gattagatct tgggtcagaa 180
ccagggggcac agctttgact gaaatattca tcaaatttgc aggagcccgt ctggttgaag 240
agcaagccca tggg 254

<210> 17
<211> 229
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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tctagcttca gtcacaggct tacgtttgcc atcgaggcac agcaacgcaa agtctgcaag 180
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<210> 18
<211> 210
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 18
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agtaatgcct ggcacatact gtggtcccaa atatttttca tatgttgttt tgccatggag 120
tctggcaaga cactcagtgt tgcattgaa caaaaggttt ttggtttcag actggaataa 180
gcaaaacttg tccgggcagt cagatccatt 210

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 19

ggatccatgg gccgtaggag aaggagtgtt

30

<210> 20

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 20

gagctcttac ttccttagga attcacag

28

<210> 21

<211> 1367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

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ttttaaggca	attaagcatg	tttgataaaa	tatatatatt	gttataaata	cttttcaaaa	180
gtataaagtt	gatgatggcg	tggtggtaga	ttatttttagt	tctaggttcg	aatgcaagtt	240
ggttttagaca	tttagcctta	ttcttttttc	taacccaaaat	aatgtaaat	ggaaaacctt	300
taggaaaaaaa	aagaaatcaa	aattgaaaac	atcatccggt	ggagtcgaga	agcccacacc	360
cacgtgaccc	aacaatatta	aaataagagt	ttgctctaca	gtaaatgcga	tactttttta	420
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catataatat	ataggggttta	gaatgccaat	ttttaaaaaa	agaataaaaa	aataaataga	780
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tgaccaaacac	ggccaaaaga	aaagagaatc	tcatcccgtt	cacacttagc	cacttaaagc	1260
tagccaaacg	gtgatctttc	tctatatatt	gtagctctct	aacacaacca	acactaccat	1320
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<210> 22

<211> 962

<212> DNA

<213> Artificial Sequence

<220>

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<400> 22

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ataatatatt tatattttta tatctattct tatgtatttt ttaaaaatct attatatatt 180
gatcaactaa aatattttta tatctacact tattttgcat ttttatcaat tttcttgctg 240
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atattgttgg aaccatatga agtggttcatt gcatttgact atgtggatag tgttttgatc 360
catgcccttc atttgccgct attaattaat ttggtaacag attcgttcta atcagttact 420
taatccttcc tcatcataat taatctggta gttcgaatgc cataatattg attagttttt 480
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catagcaatg tctaagttca taaaattcaa acaaaaaacgc aatcacacac agtggacatc 600
acttatccac tagctgatca ggatcgccgc gtcaagaaaa aaaaactgga ccccaaaagc 660
catgcacaac aacacgtact cacaaaggcg tcaatcgagc agcccaaaac attcaccaac 720
tcaacccatc atgagcccac acatttggtt tttctaacc aacctcaaac tcgtattctc 780
ttccgccacc tcatttttgt ttatttcaac acccgtaaaa ctgcatccca ccccgaggcc 840
aaatgttcat gcatgttaac aagacctatg actataaata tctgcaatct cggcccaagt 900
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ct

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<210> 23

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic human lactoferrin

<400> 23

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Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln
      35             40             45

Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly Phe
      50             55             60

Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala Ala
      65             70             75             80

Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val
      85             90             95

Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly
      100            105            110

Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val
      115            120            125

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Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu
 130 135 140
 Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro
 145 150 155 160
 Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly
 165 170 175
 Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser
 180 185 190
 Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala
 195 200 205
 Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu
 210 215 220
 Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val
 225 230 235 240
 Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val
 245 250 255
 Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu
 260 265 270
 Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln
 275 280 285
 Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser
 290 295 300
 Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr
 305 310 315 320
 Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu
 325 330 335
 Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly
 340 345 350
 Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly
 355 360 365
 Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu
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 Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val
 385 390 395 400
 Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr
 405 410 415
 Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro
 420 425 430

Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser
 435 440 445
 Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val
 450 455 460
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 Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu
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 Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly
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 Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys
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 Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu
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 Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu
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 Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn
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 Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys
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 Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile
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